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HBJDZ49	9502	847928	AC004980	42360	1-517 1224-1740 1770-2298 2337-6170 6407-6441 6816-15196
HBJDZ49	9502	847928	AC005073	42361	1-1715 2222-2480 2882-3799 5384-5472 5637-5940 6637-7520 7849-8274 8396-11766 11769-12006 12486-12589 12647-12760 12798-13105 13347-14042 14076-14293 14296-17861 17923-18121 18344-21676
HBJDZ49	9502	847928	AC018720	42362	1-88 295-1846 3509-3598 3764-4061 4797-5399 6020-6423 6565-7094 7133-10962 11199-11233 11406-16414 16433-20188
HBJDZ49	9502	847928	AC006480	42363	1-824 1727-2250 3167-3348 3382-3733 4181-4664 4957-5496 5585-5810 5829-6140 6329-6722 7752-8250 9690-10562 10591-11432 12438-12751 14763-15319 15478-15667 16874-16955 20911-21344 21469-21617

					22041-22247 25096-25193 25336-25751 26609-26714 26798-27211 28295-28832 29914-30366 31336-31510 31520-32202 33873-33965 34131-34431 34675-34784 35103-35705 36242-36731 36873-37401 37440-37680 37699-41271 41712-50442
HBJDZ49	9502	847928	AF030453	42364	1-64 232-342 1337-1852 2559-2964 3673-7264 7293-7508 7746-7780 7953-18188
HBJDZ49	9502	847928	AC004867	42365	1-1716 2250-2502 2834-3813 5396-5483 5650-5950 6624-7332 7837-8257 8379-11753 11756-12384 12781-13088 13239-13304 13326-17824 17886-18086 18320-21988 22072-23613
HBJDZ49	9502	847928	AC005088	42366	1-91 259-371 1378-1894 2601-3006 3715-7552 7788-7822 7995-12991 13010-18252
HBJDZ49	9502	847928	AC005488	42367	1-1525 2823-3802 5381-5467 5634-5934 7010-7619 7948-8368 8868-11864 11870-12107

					12594-12811 12884-13191 13225-13414 13437-14521 14529-17110 17190-17916 17924-21107 21551-23569 23842-24790 25294-25593 25666-26072 27692-27800 27845-28102 28538-29666 30322-30463 30913-31471 33356-33443 33610-33910 34799-35052 35063-35484 36553-37367 38056-39110
HBJDZ49	9502	847928	AC005098	42368	1-1716 2360-2501 2897-3814 5395-5482 5649-5949 6624-7332 7837-8257 8530-11755 11758-12386 12495-12713 12792-13099 13250-13315 13337-17835 17902-18103 18336-22003 22097-24218
HBJDZ49	9502	847928	AC004166	42369	1-1716 2357-2498 2831-3810 5393-5480 5647-5947 6621-7329 7834-8254 8376-11750 11753-12381 12778-13085 13236-13301 13323-16669 16700-17821 17883-18016 18317-21985 22062-23603
HBJDZ49	9502	847928	AC005071	42370	1-1715 2229-2480 2882-3799

					5384-5472 5637-5962 6637-7520 7764-8274 8396-12010 13347-14042 14076-14293 14296-17861 17931-18121 18344-21358
HBJDZ49	9502	847928	AC061712	42371	1-103 1368-1977 2306-2726 2999-6224 6227-6464 6951-7168 7241-7548 7582-7771 7794-10119
HBJDZ49	9502	847928	AC007000	42372	1-2261 2328-3085 3093-6210 6306-6555 6630-8724 9378-10405 10433-10732 10766-11172 11591-11805 12605-13216
HBJDZ49	9502	847928	AC006995	42373	1-719
HBJDZ49	9502	847928	AC073967	42374	1-528
HBJDZ49	9502	847928	AC006014	42375	1-979
HBJDZ49	9502	847928	AC007003	42376	1-614
HBJDZ49	9502	847928	AC007000	42377	1-35 200-361 374-4630 4674-5056 5071-7020
HBJDZ49	9502	847928	AC073517	42378	1-583
HBJDZ49	9502	847928	AC006995	42379	1-1659
HBJDZ49	9502	847928	AC006014	42380	1-929 1161-4487 4579-5506 5664-5765 5979-9483 10048-10856 11336-11702 12041-12251 12253-12463 13816-13903 13917-14426
HBJDZ49	9502	847928	AC004878	42381	1-255
HBJDZ49	9502	847928	AC004878	42382	1-741 818-1073 1163-3038
HBJDZ49	9502	847928	AC004980	42383	1-293
HBJDZ49	9502	847928	AC004980	42384	1-1417

HBJDZ49	9502	847928	AC005073	42385	1-513 2138-2341 2878-3828 4039-4407 4438-5711 6598-6908 6969-7501 7547-7645 7882-8496 8569-9146 9288-11595 11642-11927 12146-12299 12591-12757 13029-13369 13719-14460 14563-14623 14696-15271 15352-16582 16831-17249 17276-17914 17947-18016 18327-19493 19719-20635 21271-22015 22432-22985 23034-23359 24795-25234 26499-26923 27475-28264 28742-29110 29565-29655 29657-29867 30539-30779 31272-31718
HBJDZ49	9502	847928	AC005073	42386	1-257
HBJDZ49	9502	847928	AC018720	42387	1-1380
HBJDZ49	9502	847928	AC006480	42388	1-1207
HBJDZ49	9502	847928	AC006480	42389	1-327
HBJDZ49	9502	847928	AF030453	42390	1-583
HBJDZ49	9502	847928	AF030453	42391	1-3119 3130-4112
HBJDZ49	9502	847928	AC004867	42392	1-868 1145-2855 2954-4494 4586-5798 5910-9476 10040-10848 11092-11171 11330-11695 12154-12509 13065-13372 13935-14448
HBJDZ49	9502	847928	AC004867	42393	1-583 834-1954
HBJDZ49	9502	847928	AC005088	42394	1-583
HBJDZ49	9502	847928	AC005088	42395	1-3121

					3128-4110
HBJDZ49	9502	847928	AC005488	42396	1-867 1144-2852 2949-4487 4579-5789 5978-9485 10048-10911 11334-11700 12034-12509 13205-13321 13907-14417
HBJDZ49	9502	847928	AC005488	42397	1-735 738-975
HBJDZ49	9502	847928	AC005098	42398	1-866 1143-2850 2949-4489 4581-5793 5905-8184 8255-9460 10026-10834 11078-11157 11307-11672 12131-12486 13183-13299 13912-14426
HBJDZ49	9502	847928	AC005098	42399	1-937
HBJDZ49	9502	847928	AC004166	42400	1-868 1146-2858 2957-4497 4589-5801 5913-9479 10043-10851 11095-11174 11333-11698 12157-12512 13938-14451
HBJDZ49	9502	847928	AC004166	42401	1-583 834-1954
HBJDZ49	9502	847928	AC005071	42402	1-896
HBJDZ49	9502	847928	AC061712	42403	1-1123 1396-3493 3581-3836 3838-7040 7048-8923
HBJDZ49	9502	847928	AC005071	42404	1-513 2138-2341 2878-3828 4039-4407 4438-5711 6609-6900 6969-7501 7547-7645 7882-8496 8569-9146 9288-11595 11642-11927 12146-12299

					12591-12757 13029-13369 13719-14460 14563-14623 14709-15271 15352-16582 16831-17249 17276-17914 17947-18016 18327-19493 19719-20635 21586-21816 24795-25126 26501-26923 27475-28264 28742-29110 29565-29655 29657-29867 31272-31718
HBJDR24	9503	677407	AC009951	42405	1-642
HBJDR24	9503	677407	AC009951	42406	1-327
HBJDR24	9503	677407	AC009951	42407	1-486 993-1122
HBJDQ86	9504	784654	AL133548	42408	1-50 3009-3073 4198-4253 5692-5831 6776-6827 8851-8970 9968-10050 12598-12974 13262-13364 16417-16776 19112-20566
HBJDQ86	9504	784654	AL133548	42409	1-1017
HBJDM70	9505	757435	AC010894	42410	1-380
HBJDM70	9505	757435	AC010894	42411	1-502
HBJDL24	9506	678272	AC008675	42412	1-996
HBJDL24	9506	678272	AC008675	42413	1-300
HBJCQ65	9508	876430	AF192303	42414	1-1230 1271-3810
HBJCJ82	9509	779645	AL161456	42415	1-1118
HBJCJ82	9509	779645	AL158075	42416	1-1523
HBJCJ82	9509	779645	AL158075	42417	1-853 1340-2553
HBJCJ82	9509	779645	AL158075	42418	1-482
HBJCE07	9510	954090	AC025605	42419	1-357 443-919
HBJCE07	9510	954090	AC073101	42420	1-357
HBJCE07	9510	954090	AC025605	42421	1-653
HBJCE07	9510	954090	AC073101	42422	1-233
HBJCE07	9510	954090	AC073101	42423	1-420
HBJBR04	9512	847952	AC005682	42424	1-458
HBJBR04	9512	847952	AC005682	42425	1-373
HBJAP95	9513	796659	AL138715	42426	1-1044
HBJAP95	9513	796659	AL031601	42427	1-590 1338-1600

					2644-3247
HBJAP95	9513	796659	AL138715	42428	1-717
HBJAP95	9513	796659	AL138715	42429	1-265
HBJAP95	9513	796659	AL031601	42430	1-706
HBJAJ49	9515	723164	AC078846	42431	1-416
					1103-1882
HBJAJ49	9515	723164	AC078846	42432	1-116
HBJAH27	9517	682941	AC016325	42433	1-69
					560-632
					2298-2395
					2510-2613
					3563-3801
					5031-5598
					5763-5801
HBJAE32	9518	699695	AC044843	42434	1-487
					983-1447
HBJAE32	9518	699695	AC008525	42435	1-487
					983-1447
HBJAE32	9518	699695	AC008525	42436	1-337
HBJAB49	9520	722195	AF276759	42437	1-1613
HBJAB49	9520	722195	AC019031	42438	1-1613
HBJAB49	9520	722195	AF276759	42439	1-561
HBJAB49	9520	722195	AC019031	42440	1-561
HBJAB28	9521	847966	AC023071	42441	1-736
HBJAB15	9522	660552	AP001931	42442	1-1266
HBJAB15	9522	660552	AP000727	42443	1-1264
HBJAB15	9522	660552	AP001931	42444	1-366
HBJAB15	9522	660552	AP001931	42445	1-308
HBJAB15	9522	660552	AP000727	42446	1-366
HBJAB15	9522	660552	AP000727	42447	1-308
HBD4E47	9523	720008	AL353776	42448	1-1591
HBD4E47	9523	720008	AL353776	42449	1-490
HBDAD16	9525	661560	AC013396	42450	1-1371
HBDAD16	9525	661560	AC013396	42451	1-296
HBDAD16	9525	661560	AC013396	42452	1-204
HBCCO10	9526	963157	AC009634	42453	1-575
HBCCO10	9526	963157	AC011721	42454	1-575
HBCCO10	9526	963157	AC009634	42455	1-206
HBCCO10	9526	963157	AC011721	42456	1-206
HBCCO10	9526	963157	AC011721	42457	1-86
HBCCJ05	9527	930956	AC068322	42458	1-600
HBCCJ05	9527	930956	AC027243	42459	1-600
HBCCJ05	9527	930956	AC024059	42460	1-600
HBCCJ05	9527	930956	AC010868	42461	1-584
HBCCJ05	9527	930956	AC068322	42462	1-424
HBCCJ05	9527	930956	AC027243	42463	1-456
HBCCJ05	9527	930956	AC068322	42464	1-460
					1112-1585
HBCCJ05	9527	930956	AC027243	42465	1-460
					1112-1585
HBCCJ05	9527	930956	AC024059	42466	1-456
HBCCJ05	9527	930956	AC010868	42467	1-385
HBCCJ05	9527	930956	AC010868	42468	1-335
HBCCD06	9529	938319	AC007783	42469	1-2334
					2508-3084
					3578-3890

					4198-4294 4376-4623 4712-5349 5369-6088 6527-7107 7298-7392 7730-7846 9147-9476 10487-10575 10791-11298 11485-11601 11783-13009 13207-13501 13540-13772 14439-14800 14923-14983 15133-15355 15485-15653 16750-16805 16894-17078 17162-17219 18003-18089 21085-21146 21358-21501
HBCCD06	9529	938319	AC007783	42470	1-308
HBCCD06	9529	938319	AC007783	42471	1-1024
HBCCB51	9530	975256	AL139353	42472	1-71 265-794 1791-2077 2409-2656
HBCBN51	9532	952057	AC073846	42473	1-141 323-951 1073-1625 1640-2371
HBCBN51	9532	952057	AC073846	42474	1-285
HBCBF12	9535	969578	AC068735	42475	1-530
HBCBF12	9535	969578	AC021725	42476	1-534
HBCBF12	9535	969578	AL021368	42477	1-382 762-1102 1231-1761
HBCBF12	9535	969578	AC068735	42478	1-342
HBCBF12	9535	969578	AC021725	42479	1-342
HBCBF12	9535	969578	AC068735	42480	1-659
HBCBF12	9535	969578	AC021725	42481	1-679
HBCBF12	9535	969578	AL021368	42482	1-664
HBCBF12	9535	969578	AL021368	42483	1-307
HBCBE57	9536	848322	AL031666	42484	1-1235
HBCBE57	9536	848322	AL031666	42485	1-508
HBCBE57	9536	848322	AL031666	42486	1-648
HBCBB22	9537	848325	AC010735	42487	1-900
HBCAT10	9539	968195	AL357521	42488	1-374
HBCAT10	9539	968195	AL021528	42489	1-374
HBCAT10	9539	968195	AL357521	42490	1-689
HBCAT10	9539	968195	AL357521	42491	1-355
HBCAT10	9539	968195	AL021528	42492	1-689
HBCAT10	9539	968195	AL021528	42493	1-355

HBCAS32	9540	699489	AC007101	42494	1-215 867-1214 1226-2260 2359-2415
HBCAQ85	9541	783431	AC019071	42495	1-831 1116-1365 1600-1920 2161-2334 2902-3156 3364-3836 4074-4278 4306-4417 4485-4581 4693-4853 4995-5264 5758-5863 6411-6509 6551-6922
HBCAQ85	9541	783431	AC019071	42496	1-412
HASCG58	9543	738423	AC011116	42497	1-869
HASCG58	9543	738423	AC078794	42498	1-870
HASCG58	9543	738423	AC011116	42499	1-971
HASCG58	9543	738423	AC078794	42500	1-623
HASCG58	9543	738423	AC011116	42501	1-623
HASAW90	9544	789112	AC010234	42502	1-2931
HASAW90	9544	789112	AC021464	42503	1-58 332-547 909-1209 2280-2634 3445-3539 4477-4620 7577-10496 12087-13447 13462-15091 15142-16137
HASAW90	9544	789112	AC021464	42504	1-506
HASAC10	9546	968746	AC007677	42505	1-477
HASAC10	9546	968746	AC007677	42506	1-1410

[052] Table 1B summarizes additional polynucleotides encompassed by the invention (including cDNA clones related to the sequences (Clone ID NO:Z), contig sequences (contig identifier (Contig ID:) contig nucleotide sequence identifiers (SEQ ID NO:X)), and genomic sequences (SEQ ID NO:B). The first column provides a unique clone identifier, "Clone ID NO:Z", for a cDNA clone related to each contig sequence. The second column provides the sequence identifier, "SEQ ID NO:X", for each contig sequence. The third column provides a unique contig identifier, "Contig ID:" for each contig sequence. The fourth column, provides a BAC identifier "BAC ID NO:A" for the BAC clone referenced in the corresponding row of the table. The fifth column provides the nucleotide sequence identifier, "SEQ ID NO:B" for a fragment of the BAC clone identified in column four of the corresponding row of the table. The sixth column, "Exon From-To", provides the location (i.e., nucleotide position numbers) within the polynucleotide sequence of SEQ ID NO:B which delineate certain polynucleotides of the invention that are also exemplary members of polynucleotide sequences that encode polypeptides of the invention (e.g., polypeptides containing amino acid sequences encoded by the polynucleotide sequences delineated in column six, and fragments and variants thereof).

TABLE 2

Clone ID NO:Z	Contig ID:	SEQ ID NO:X	Analysis Method	PFam/NR Description	PFam/NR Accession Number	Score/ Percent Identity	NT From	NT To
HAMHB21	961376	11	HMMER 2.1.1	PFAM: RhoGAP domain	PF00620	100	497	916
HBDAC79	935414	26	HMMER 2.1.1	PFAM: Acyl-CoA dehydrogenase	PF00441	102.6	94	342
			blastx.14	(AL021958) fadE9 [Mycobacterium tuberculosis]	gi 2911026 emb CAA 17519.1	62% 51% 64% 35%	94 250 348 6	255 384 422 89
HBJAG72	722723	32	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	2.32	83	115
HBJGT92	919507	107	HMMER 1.8	PFAM: Bacterial mutT protein	PF00293	7.68	377	436
HBJIY20	669519	141	HMMER 2.1.1	PFAM: Orn/Lys/Arg decarboxylase	PF01276	53.1	49	162
HBMBU24	677240	234	HMMER 1.8	PFAM: Core histones H2A, H2B, H3 and H4	PF00125	7.72	139	192
HBMZ71	880580	238	HMMER 1.8	PFAM: von Willebrand factor type D domain	PF00094	26.52	200	526
HBMDC16	888206	258	blastx.2	Butyrophilin-like protein BUTR-1.	sp AAF72554 AAF72 554	50%	19	315
HBMUO90	928078	294	blastx.14	Zfp61p [Mus musculus]	gi 887887 gb AAC52 290.1	84% 53%	24 154	119 243
HBMXE31	573323	317	HMMER 1.8	PFAM: Gonadotropin- releasing hormones	PF00446	10.78	112	141
HCFCF47	894415	372	HMMER 1.8	PFAM: Eukaryotic protein kinase domain	PF00069	89.54	20	295
HCFCJ21	671028	374	HMMER	PFAM: Core histones	PF00125	12.79	123	188

HCFLE95	945122	391	1.8 blastx.14	H2A, H2B, H3 and H4 p34 protein [Rattus sp.]	gi 534876 dbj BAA02786.1	81% 100% 85%	126 236 71	191 271 91
HCUAL07	953876	449	blastx.14	(AF079098) arginine-tRNA-protein transferase 1-1p; ATE1-1p [Homo sapiens]	gi 3806094 gb AAD12366.1	87%	5	97
HCUBJ11	967484	478	blastx.14	Ps 2=basic proline-rich protein(PRB1L precursor 1 1 [Homo sapiens]	gi 386433 gb AAB27289.1	37% 53% 35% 40% 28% 40% 36% 36% 41% 41% 32% 33% 36% 36% 71% 71% 35%	158 62 325 133 158 133 225 225 74 74 325 158 158 183 44 44 74	63 24 242 59 63 59 160 160 24 24 242 87 93 118 24 24 24
HCUDT65	915742	548	HMMER 2.1.1 blastx.14	PFAM: tRNA synthetases class II (A) ORF YNL040w [Saccharomyces cerevisiae]	PF01411 gi 1301892 emb CAA95907.1	35.1 42% 52% 31% 42%	697 763 658 1153 1678	930 972 759 1293 1740

HCUEU10	964857	595	HMMER 1.8		PFAM: Bacterial regulatory proteins, luxR family	PF00196		21% 20% 5.43	1009 1273 13	1149 1494 42
HCUGB48	880730	647	HMMER 1.8		PFAM: TNFR/NGFR cysteine-rich region	PF00020		7.99	173	226
HCUGR38	706471	670	HMMER 1.8		PFAM: Alcohol/other dehydrogenases, short chain type	PF00106		73.02	102	284
HCUHM44	615198	702	HMMER 1.8		PFAM: HMG (high mobility group) box	PF00505		4.81	2	73
HCWAK80	702435	748	HMMER 1.8		PFAM: Src homology domain 3	PF00018		3.55	316	387
HCWAR05	932623	759	blastx.14		hypothetical protein [Synechocystis sp.]	gi 1653272 dbj BAA1 8187.1		47% 46% 71%	235 70 321	83 32 301
HCWBB63	667283	782	HMMER 2.1.1		PFAM: Secretory protein of YscJ/FliF family	PF01514		78.2	45	275
HCWBE76	968515	799	HMMER 1.8		PFAM: Helix-loop-helix DNA-binding domain	PF00010		9.77	13	51
HCWBI37	967717	809	blastx.14		URF (pot. 4.5S protein) [Escherichia coli]	gi 42759 emb CAA25 537.1		63% 85% 60%	9 202 228	179 222 257
HCWBI53	934909	810	blastx.14		lepA [Mycobacterium tuberculosis]	gi 1655655 emb CAB 03723.1		85% 84%	65 9	166 65
HCWBI90	921653	812	blastx.14		xylose isomerase [Klebsiella pneumoniae]	gi 43952 emb CAA43 389.1		59% 55%	316 344	8 291
HCWBN06	924638	825	blastx.14		collagen type XVII [Mus musculus]	gi 309183 gb AAA37 443.1		26% 46%	153 262	266 306

HCWBQ03	920886	834	blastx.14	ORF YBR208c [Saccharomyces cerevisiae]			57%	5	46
							36%	75	140
							46%	259	303
							43%	310	357
							75%	337	360
							42%	78	119
HCWCM65	529230	891	HMMER 1.8	PFAM: AMP-binding enzymes	gi 536588 emb CAA8 5172.1		69.62	31	264
HCWCR31	693632	909	HMMER 2.1.1	PFAM: ATP synthase (E/31 kDa) subunit	PF01991		80	229	381
HCWDI64	924632	945	blastx.14	tetracycline transporter- like protein [Mus musculus]	gi 2506078 dbj BAA2 2622.1		82%	117	167
							87%	73	120
HCWDJ23	527555	952	HMMER 2.1.1	PFAM: Bacterial extracellular solute- binding proteins, family 3	PF00497		27.3	25	198
HCWDL45	889416	957	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099		4.63	121	168
HCWDR01	839104	973	HMMER 1.8	PFAM: ABC transporters	PF00005		62.98	15	179
			blastx.2	(AE000411) putative ATP-binding component of a transport system [Escherichia coli]	gb AAC76377.1		69%	9	215
							44%	18	200
							51%	281	373
							41%	391	477
HCWDV17	974478	993	HMMER 1.8	PFAM: Bacterial regulatory proteins, luxR family	PF00196		81.59	416	613
HCWDX22	967361	1014	blastx.14	copC peptide	gi 151190 gb AAA25		79%	365	84

HCWDX76	932614	1019	blastx.14	[Pseudomonas syringae] (AF102543) unknown [Zymomonas mobilis]	808.1 gi 4378174 gb AAD1 9419.1	81%	423	358
HCWED61	971865	1041	blastx.14	gp210 (AA 1-1886) [Rattus norvegicus]	gi 56463 emb CAA68 759.1	75%	481	212
HCWEG69	948693	1058	HMMER 1.8 blastx.14	PFAM: Zinc-binding metalloprotease domain. orf3 [Pseudomonas aeruginosa]	PF00099	2.79	57	98
HCWEI19	948690	1066	HMMER 1.8 blastx.14	PFAM: Zinc-binding metalloprotease domain formaldehyde dehydrogenase (glutathione) [Escherichia coli]	gi 557259 emb CAA5 7572.1 PF00099	55% 87%	248 56	45 9
HCWEL01	916972	1086	blastx.14	(AF010496) exonuclease SbcD homolog [Rhodobacter capsulatus]	gi 887431 emb CAA5 2057.1	75%	300	10
HCWEM51	920887	1096	blastx.14	argininosuccinate lyase [Bacillus subtilis]	gi 3128267 gb AAC1 6119.1	39% 47%	34 193	171 249
HCWEQ14	908245	1105	HMMER 1.8 blastx.14	PFAM: DEAD and DEAH box helicases (AC002985) R27090_2 [Homo sapiens]	gi 2635409 emb CAB 14904.1 PF00270	54% 47%	365 57	39 7
HCWEW45	571355	1116	HMMER 1.8 blastx.14	PFAM: Heat shock hsp90 proteins	PF00183	72.08	37	177
HCWEY34	954142	1125	blastx.14	(AJ000758) precorrin-4 methylase [Bacillus megaterium]	gi 2443870 gb AAB8 1544.1 gi 3724045 emb CAA 04314.1	100% 66%	37 5	177 40
						10.32	37	186
						32%	3	242

HCWFF88	506577	1143	HMMER 1.8	PFAM: Src homology domain 3	PF00018	4.92	140	181
HCWFK57	861907	1149	HMMER 2.1.1	PFAM: RNA polymerase beta subunit	PF00562	36.2	34	270
HCWFT29	690751	1186	HMMER 1.8	PFAM: Helicases conserved C-terminal domain	PF00271	4.51	105	152
HCWFU66	853005	1196	HMMER 2.1.1	PFAM: Aldehyde dehydrogenase family	PF00171	71.4	105	269
HCWGB78	861843	1217	HMMER 2.1.1	PFAM: Ribosomal protein L31	PF01197	50.8	126	236
HCWGE12	967067	1223	HMMER 1.8	PFAM: Bacterial mufT protein	PF00293	4.04	214	288
HCWGW12	964088	1262	blastx.14	L-lactate dehydrogenase (EC 1.1.1.27) - Acinetobacter 1	pir A37334 A37334	73%	137	60
HCWGY90	960159	1288	HMMER 1.8	PFAM: Bacterial regulatory helix-loop- helix proteins, araC family	PF00165	58.7	6	137
			blastx.14	operon regulatory protein [Erwinia carotovora]	gi 48382 gb AA24 811.1	86%	6	158
HCWHB12	970688	1295	blastx.14	Nodulation protein V (EC 2.7.3.-). [Escherichia coli]	gi 1736771 dbj BAA1 5920.1	47% 33% 85%	195 59 310	314 211 330
HCWHD07	953384	1305	blastx.14	Isp42p [Saccharomyces cerevisiae]	gi 736300 emb CAA8 8644.1	41% 46% 50%	56 298 341	301 393 394
HCWHP74	598510	1334	HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding domain	PF00130	2.09	68	112

HCWHQ03	924187	1336	blastx.14	(AL049608) extensin-like protein [Arabidopsis thaliana]	gi 4584539 emb CAB40769.1	50%	85	14 206 126 253 247 218
HCWHQ31	574945	1337	HMMER 2.1.1	PFAM: Carbon-nitrogen hydrolase	PF00795	39.4	141	308
HCWHR81	935419	1343	HMMER 2.1.1	PFAM: Ribosomal protein L30p/L7e	PF00327	90.5	107	265
HCWHT59	924105	1349	blastx.14	(AF047828) syringomycin synthetase [Pseudomonas syringae pv. syringae]	gi 3510629 gb AAC80285.1	57% 45% 50% 50% 36% 34% 61% 55% 40% 33% 66% 55% 26% 26% 44% 41% 41% 33% 22% 32%	261 327 261 261 122 122 329 157 104 104 107 142 305 249 249 305 157 157 311 107 246	148 148 148 148 9 9 252 104 9 9 252 104 9 9 107 252 160 160 252 107 107 249 15 163
HCWK08	959388	1388	blastx.14	pot. ORF 1 [Homo]	gi 1335196 emb CAA	57%	83	27

				sapiens]	26917.1]	62%	303	256
HCWKN08	959380	1409	blastx.14	CeoB [Burkholderia cepacia]	gi 2109271 gb AAB5 8161.1	32% 47%	192 247	82 179
HCWKV68	959801	1427	blastx.14	(AL121600) hypothetical protein SCF76.09 1	gi 6002364 emb CAB 56729.1	55% 50% 62% 54%	249 148 281 61	169 83 258 29
HCWLD06	935392	1437	blastx.14	ORF_o485 [Escherichia coli]	gi 887832 gb AAA83 063.1	34% 42% 57%	219 120 238	142 43 218
HCWLE37	960093	1442	blastx.14	(AF039571) peripheral benzodiazepine receptor interacting protein; PBR-IP/PRAX1 [Homo sapiens]	gi 4104812 gb AAD1 1957.1	47% 42% 35%	240 449 66	7 282 7
HCWLH79	959458	1453	blastx.14	(AC004877) sco-spondin-mucin-like; similar to p98167 1 sapiens]	gi 3638957 gb AAC3 6301.1	100% 85% 87% 44% 36%	126 304 103 66 250	263 345 126 119 315
HCWTB11	965024	1462	blastx.14	DNA primase [Escherichia coli]	gi 147755 gb AAA24 600.1	27% 71%	289 326	191 306
HCWTB56	853009	1470	HMMER 1.8	PFAM: E1-E2 ATPases	PF00122	45% 55.15	341 2	3 301
			blastx.2	cadmium resistance protein [Lactococcus lactis]	gb AAB37345.1	42%	2	316
HCWTR08	958791	1516	blastx.14	(AE000888) malate dehydrogenase [Methanobacterium	gi 2622314 gb AAB8 5694.1	43% 44%	66 182	134 262

HCWTR54	729290	1517	HMMER 1.8	thermoautotroph[icum] PFAM: Helicases conserved C-terminal domain	PF00271	6.14	151	198
HCWTS15	654317	1519	HMMER 1.8	PFAM: D-isomer specific 2-hydroxyacid dehydrogenases	PF00389	47.52	2	166
HCWUU16	661570	1593	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	2.17	33	77
HDDMA83	926991	1633	blastx.14	(AF038963) RNA helicase [Homo sapiens]	gi 4405795 gb AAD1 9826.1	100% 51% 100% 90%	2 537 656 526	514 635 694 558
HDMAQ15	941282	1646	HMMER 2.1.1 blastx.2	PFAM: POT family	PF00854	77.2	811	386
HDPAG32	947832	1655	HMMER 2.1.1	(AF121080) cAMP inducible 1 protein [Mus musculus]	gb AAD24570.1 AF1 21080_1	80%	2	997
HDPCN94	794275	1678	HMMER 2.1.1	PFAM: Peptidase family M1	PF01433	39.1	335	577
HDPFF07	974494	1694	blastx.14	PFAM: RhoGEF domain	PF00621	54.2	363	740
HDPIT53	926498	1736	blastx.14	(AF151363) Cdc42 GTPase-activating protein [Mus musculus]	gi 5020264 gb AAD3 8043.1 AF151363_1	92% 96% 50%	513 715 458	716 789 505
HDPIT61	741724	1737	blastx.2	(AF109719) BAT2 [Mus musculus]	gi 3941737 gb AAC8 2480.1	50% 30%	229 278	170 219
				(AF121080) cAMP inducible 1 protein [Mus musculus]	gb AAD24570.1 AF1 21080_1	73% 57%	48 293	329 397

HDPKD52	959653	1750	HMMER 1.8	PFAM: Fibronectin type III domain	PF00041	4.82	340	402
HDPLC45	909091	1755	HMMER 2.1.1	PFAM: BTB/POZ domain	PF00651	39.5	280	507
HDPMA48	582015	1775	blastx.2	(AF038007) FIC1 [Homo sapiens]	gb AAC63461.1	54%	152	703
HDPMO62	912722	1780	HMMER 1.8	PFAM: Ras family (contains ATP/GTP binding P-loop)	PF00071	132.39	127	432
			blastx.2	rab-related GTP-binding protein [Homo sapiens]	emb CAA68227.1	54% 57%	133 20	444 76
HDPNC96	934520	1788	HMMER 1.8	PFAM: Eukaryotic protein kinase domain	PF00069	206.63	3	734
			blastx.14	HUMAN NDR [unidentified]	gi 2304746 emb CAA 03387.1	92%	3	734
HDPOJ93	792193	1797	HMMER 1.8	PFAM: EF hand	PF00036	7.78	266	313
HDPPP24	812091	1815	HMMER 2.1.1	PFAM: Fes/CIP4 homology domain	PF00611	22.4	151	387
HDPPU44	951276	1818	HMMER 1.8	PFAM: Lectin C-type domain short and long forms	PF00059	37.49	245	376
HDPRH02	919404	1837	blastx.14	ORF YGR090w [Saccharomyces cerevisiae]	gi 1323133 emb CAA 97093.1	30% 48%	266 593	451 673
			blastx.14	reverse transcriptase [Homo sapiens]	gi 439877 gb AAB02 291.1	66% 37% 54%	6 280 235	59 351 267
HDPTW90	722699	1868	HMMER 1.8	PFAM: IG (immunoglobulin)	PF00047	3.32	1	24

HDPVG11	966556	1877	HMMER-1.8	superfamily PFAM: PH (pleckstrin homology) domain	PF00169	16	518	613
HDPWE80	909916	1890	HMMER-2.1.1 blastx.2	PFAM: PH domain (AF102854) membrane-associated guanylate kinase-interacting protein 2 Maguin-2 [Rattus norvegicus]	PF00169 gb AAD04568.1	81.2 36%	412 349	708 756
HDPWY46	915964	1894	blastx.14	(AF061738) leucine aminopeptidase [Homo sapiens]	gi 4335941 gb AAD17527.1	94% 87% 80% 95% 62% 33%	3 316 140 254 425 305	152 438 217 316 472 358
HDQEF04	927024	1914	blastx.14	Bassoon [Mus musculus]	gi 3413810 emb CAA76598.1	75%	239	216
HDQGT70	909848	1936	blastx.14	Bat2 [Homo sapiens]	gi 29375 emb CAA78744.1	37%	248	201
HDQHT10	963481	1944	blastx.14	(AF039571) peripheral benzodiazepine receptor interacting protein; PBR-IP/PRAX1 [Homo sapiens]	gi 4104812 gb AAD11957.1	58% 43% 100% 55% 42% 58% 83%	490 387 76 253 256 45 51	455 319 59 227 215 10 34
HDQHZ10	961336	1945	blastx.14	fractionated X-irradiation-induced 29 thymoma [Mus musculus]	gi 1389694 gb AAB02905.1	51% 71%	47 2	256 43
HDQHZ22	879416	1946	blastx.2	cysteine rich hair keratin	emb CAA56339.1	40%	65	319

					associated protein [Oryctolagus cuniculus]			42%	65	352
HDTAY23	973925	1956	blastx.14		(AF086624) serine threonine kinase [Rattus norvegicus]		gi 3800869 gb AAC6 8900.1	98%	78	254
HDTAY23	974565	9561	blastx.14		(AF086624) serine threonine kinase [Rattus norvegicus]		gi 3800869 gb AAC6 8900.1	98% 85% 100% 66%	79 330 371 305	255 371 403 331
HDTBO48	945083	1959	HMMER 1.8		PFAM: IG (immunoglobulin) superfamily		PF00047	18.53	159	347
			blastx		(AJ009698) embigin protein [Rattus norvegicus]		emb CAA08796.1	58% 75% 58%	132 273 357	248 356 464
HDTBR50	846630	1968	HMMER 1.8		PFAM: Thioredoxins		PF00085	29.85	163	297
HDTBY88	934472	1973	HMMER 2.1.1		PFAM: Eukaryotic protein kinase domain		PF00069	93.6	3	302
			blastx.14		p56 KKIAMRE protein kinase [Homo sapiens]		gi 1517820 gb AAC5 0918.1	82% 35% 100%	3 192 492	170 458 509
HDTDC53	916348	1977	HMMER 1.8		PFAM: Core histones H2A, H2B, H3 and H4		PF00125	7.98	180	233
HDTEI19	912765	1984	blastx.14		rab4b [Canis familiaris]		gi 919 emb CAA3980 0.1	78% 88%	244 387	354 413
HDTES50	964709	1987	HMMER 1.8		PFAM: RNA recognition motif. (aka RRM, RBD, or RNP domain)		PF00076	31.58	108	326
			blastx.2		arginine-rich nuclear		gb AAA35554.1	65%	36	350

HDTHQ15	923899	2009	blastx.14	protein [Homo sapiens] Similar to a C.elegans protein encoded in cosmid C27F2 (U40419) [Homo sapiens]	gi 1665781 dbj BAA1 3387.1	97%	4	612
HDTHZ46	957669	2012	blastx.14	(AC004877) sco-spondin- mucin-like; similar to p98167 1 sapiens]	gi 3638957 gb AAC3 6301.1	43% 42% 46% 43% 40% 38%	100 45 172 2 5 318	168 101 216 49 49 371
HDTID61	908946	2016	HMMER 1.8	PFAM: Zinc finger, C2H2 type	PF000096	7.07	407	430
			blastx.2	(AK002053) unnamed protein product [Homo sapiens]	dbj BAA92059.1	46% 53% 50% 45% 47% 49% 46% 33% 42% 34% 51% 57% 37% 32% 50% 47% 66%	45 45 33 45 45 48 45 18 18 60 18 347 347 338 374 338 519	389 341 341 389 344 356 344 674 320 554 245 457 547 553 457 442 554
HDTIF01	883070	2017	blastx.2	(AF010144) neuronal	gb AAC08737.1	61%	315	524

					thread protein AD7c-NTP [Homo sapiens]				61%	309	509
									65%	361	507
									62%	34	162
									60%	53	172
									41%	304	507
									35%	286	507
									40%	327	473
									50%	50	151
									57%	89	166
									47%	109	171
									37%	308	379
									52%	128	178
HDTIZ44	925574	2032	blastx.14	procollagen alpha 2(V) [Homo sapiens]	gi 2370202 emb CAA 75002.1				43%	77	9
									40%	89	9
									37%	89	9
									57%	229	188
									47%	183	133
									60%	135	106
									47%	328	278
									75%	165	142
									60%	121	92
									43%	139	92
									54%	165	133
									60%	162	133
									54%	226	194
HDTIJ37	799834	2036	HMMER 1.8	PFAM: Laminin B (Domain IV)	PF00052				2.02	386	466
HDTJJ02	913787	2037	HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding domain	PF00130				5.7	21	68
HDTKQ14	886936	2044	HMMER	PFAM: Src homology	PF00018				12.87	430	546

HDTLD17	908601	2052	1.8	domain 3	emb CAB41255.1 PF00096	100%	439	555
			blastx.2	(AL049683) hypothetical protein [Homo sapiens]		56%	76	291
			HMMER 2.1.1	PFAM: Zinc finger, C2H2 type		96.3	154	222
			blastx.2	Zfp-29 [Mus musculus]	emb CAA38920.1	48%	49	636
						65%	49	399
						66%	49	399
						66%	70	399
						65%	49	411
						62%	49	369
						64%	70	381
						47%	115	636
						58%	49	324
						42%	372	641
						50%	375	569
						47%	375	569
						47%	375	569
						48%	372	569
						43%	372	578
						42%	372	602
						46%	375	569
						35%	279	569
						43%	372	569
						43%	375	569
						46%	375	569
						63%	547	636
						63%	547	636
						52%	538	651
						56%	547	642
						35%	375	491

HEOMG48	963338	2091	blastx.14	very large tegument protein [human herpesvirus 2]	gi 1869859 emb CAB06722.1	66%	641	667
HEOMG78	920911	2092	blastx.14	contains similarity to C2 domains [Caenorhabditis elegans]	gi 1825586 gb AAB42222.1	70% 40%	294 136	437 246
HEOMS08	959581	2113	blastx.14	(AF034970) docking protein [Homo sapiens]	gi 3043919 gb AAC13265.1	93% 83%	129 172	173 207
HEOMT79	936687	2118	blastx.14	(AF108420) 1-aminocyclopropane-carboxylate synthase [Fugu rubripes]	gi 4426837 gb AAD20564.1	52%	10	210
HEOMU79	965900	2121	blastx.14	HLA-B-associated transcript 2 (BAT2) [Homo sapiens]	gi 179339 gb AAA35585.1	29%	320	198
HEOMX92	919200	2131	blastx.14	TGR-CL5bis [Homo sapiens]	gi 1247469 emb CAA01862.1	53% 38% 53% 30% 27%	274 129 271 44 206	230 91 233 6 174
HEOMX92	961148	9562	blastx.14	retrovirus-related reverse transcriptase pseudogene - slow loris	pir B25313 GNLRL1	46% 50%	44 247	241 312
HEONQ19	930705	2142	HMMER 2.1.1	PFAM: PH domain	PF00169	42.5	213	533
			blastx.2	(AJ250425) Collybistin I [Rattus norvegicus]	emb CAB65966.1	96%	9	629

HEONV59	949152	2148	blastx.2	(AK001463) unnamed protein product [Homo sapiens]	dbj BAA91707.1	51% 50%	163 284	279 379
HEOPE58	851009	2157	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	5.32	320	364
HEOPO08	958184	2174	blastx.14	alpha-1 type II collagen [Xenopus laevis]	gi 214044 gb AAA49679.1	38% 32% 31% 75% 36%	142 429 429 273 208	11 346 334 250 134
HEOQC76	909032	2189	HMMER 2.1.1 blastx.2	PFAM: Zinc finger, C2H2 type (AK001753) unnamed protein product [Homo sapiens]	PF00096 dbj BAA91884.1	86.9 37% 33% 35% 52% 29%	169 139 139 139 154 196	237 609 609 480 306 582
HEOQP44	942596	2203	HMMER 2.1.1	PFAM: Beta-lactamase	PF00144	420.7	250	1026
HEOQS11	965930	2204	blastx.14	ORF1A [Homo sapiens]	gi 475909 emb CAA47472.1	51%	30	152
HEORE79	959572	2214	blastx.14	rehydrin [Tortula ruralis]	gi 1732471 gb AAB49656.1	53% 46% 50% 50% 55% 55% 42% 62% 62% 62%	101 101 232 284 58 180 223 58 180 302	145 145 267 325 84 206 264 81 203 325

HHECO01	915285	2250	blastx.14	(AF039691) antigen NY-CO-9 [Homo sapiens]	gi 3170182 gb AAC18040.1	65% 100%	302 25	174 2
HHEEC07	952455	2267	blastx.14	(AF064257) Dhml-like protein [Homo sapiens]	gi 5881961 gb AAD55138.1 AF064257.1	99% 100%	1202 1862	1801 1912
HHEHU73	923895	2279	HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding domain	PF00130	4.1	115	156
HHEJH30	961974	2282	blastx.14	(AF180920) cyclin ania-6a [Homo sapiens]	gi 5823554 gb AAD53184.1 AF180920.1	95% 95%	226 429	417 494
HHEHD45	919630	2302	HMMER 1.8	PFAM: Double-stranded RNA binding motif	PF00035	12.86	25	114
			blastx.14	[D.melanogaster mRNA, complete cds.], gene product [Drosophila melanogaster]	gi 158506 gb AAA73062.1	52% 47%	1 235	114 297
HHEQK01	871911	2346	HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding domain	PF00130	3.27	64	90
HHEQV39	932851	2354	HMMER 1.8	PFAM: Src homology domain 3	PF00018	30.41	526	708
HHESU85	783820	2381	HMMER 1.8	PFAM: Heat shock hsp90 proteins	PF00183	11.81	88	288
HHETQ54	908567	2392	HMMER 2.1.1	PFAM: KRAB box	PF01352	166.4	233	421
			blastx.14	NK10 [Mus musculus]	gi 506502 emb CAA56225.1	89%	212	448
HHEUA62	965709	2400	HMMER 1.8	PFAM: Spectrin alpha chain, repeated domain	PF00435	10.48	103	186
			blastx.14	(AB023622) Septin6 [Mus musculus]	gi 5689158 dbj BAA82838.1	59% 60%	13 211	144 315

HHEUC31	795268	2401	HMMER 2.1.1	PFAM: Ank repeat	PF00023	31.5	3	92
HKBAT27	963724	2486	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	2.17	11	37
HLMBW11	950728	2526	blastx.14	(AF156884) RIP-like kinase [Homo sapiens]	gi 5059425 gb AAD3 9005.1 AF156884_1	92%	129	782
HLMBY16	531053	2529	HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding domain	PF00130	1.99	82	123
HLMDU71	531228	2572	HMMER 2.1.1	PFAM: Phosphate- binding protein	PF01449	48.1	1	123
HLMFU09	909666	2600	blastx.14	(AF151363) Cdc42 GTPase-activating protein [Mus musculus]	gi 5020264 gb AAD3 8043.1 AF151363_1	78%	277	372
HLMHP67	967636	2633	blastx.14	Hypothetical bacteriophage n4 receptor protein NfrA precursor. [Escherichia coli]	gi 1651236 dbj BAA3 5202.1	82% 100%	107 3	340 104
HLMHT94	531054	2641	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	2.86	264	284
HLMIX95	960056	2679	blastx.14	(AB008430) CDEP [Homo sapiens]	gi 2766165 dbj BAA2 4267.1	89% 69%	440 47	330 9
HLMMA52	920292	2694	blastx.14	ORF-3 protein [Pseudorabies virus]	gi 334072 gb AAA47 471.1	43% 100% 70%	115 165 174	162 176 203
HLMMD05	932127	2697	blastx.14	collagen [Ascaris suum]	gi 159657 gb AAA29 371.1	50% 61% 44% 58% 63% 50%	189 355 189 107 349 387	124 317 115 72 317 352

HLMMV66	926188	2733	HMMER 1.8	PFAM: Ank repeat	PF00023	42% 50% 46% 46% 32% 46%	358 407 355 110 189 355	317 366 317 66 115 317
			blastx.14	similar to HUMORFU (D26069) [Homo sapiens]	gi 488505 dbj BAA06 418.1	62% 81% 86% 71% 39% 43%	230 337 404 378 173 99	382 384 448 419 256 146
HLMNL55	964739	2769	blastx.14	dynein heavy chain isotype 6 [Tripneustes gratilla]	gi 687206 gb AAA63 589.1	70% 37%	19 184	138 231
HLMNN02	920296	2776	blastx.14	(AF083501) latent nuclear antigen [Macaca mulatta rhadinovirus 17577]	gi 4494984 gb AAD2 1406.1	36% 53% 50% 33%	345 191 86 306	289 153 57 208
HL YAA41	909874	2871	HMMER 2.1.1	PFAM: PH domain	PF00169	37.3	162	260
HL YDL60	909866	2980	blastx.14	ORF-3 protein [Pseudorabies virus]	gi 334072 gb AAA47 471.1	44% 37% 35% 30% 39% 75% 47% 75%	89 229 376 259 283 179 232 26	15 158 293 191 215 156 182 3

HL YDS11	966732	2986	blastx.14	orfIV [Borna disease virus]		gi 473842 gb AAA20666.1	38%	250	197
HL YDT68	526245	2991	HMMER 1.8	PFAM: Zinc finger, C2H2 type		PF00096	38%	223	161
HL YDV62	927872	2993	HMMER 2.1.1	PFAM: PH domain		PF00169	39%	200	3
			blastx.2	(AC005496) unknown protein [Arabidopsis thaliana]		gb AAC35236.1	4.11	89	124
HL YEN93	682176	3005	HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding domain		PF00130	58.6	188	406
HL YGP46	832311	3042	HMMER 2.1.1	PFAM: IQ calmodulin-binding motif		PF00612	41%	113	292
HL YHN67	920551	3056	blastx.14	EDTP(egg derived tyrosine phosphatase).		sp BAA33720 BAA33720	38%	451	504
HMAAF10	968199	3062	blastx.14	Formate c-acetyltransferase (EC 2.3.1.54). [Escherichia coli]		gi 1651427 dbj BAA35638.1	2.86	383	409
							100%	1	300
							76%	347	385
HMABJ56	907640	3063	HMMER 2.1.1	PFAM: ADP-ribosylation factor family		PF00025	24.4	157	231
			blastx.14	(AF082517) ADP-ribosylation factor [Entamoeba histolytica]		gi 3746799 gb AAC64063.1	39%	281	403
HMABQ71	729831	3065	HMMER 2.1.1	PFAM: DNA topoisomerase II (N-terminal region)		PF00204	56%	154	228
							61%	233	271
							128.8	210	407

HMADC02	920088	3067	blastx.14	ORF_f418 [Escherichia coli]	gi 536985 gb AAA97040.1	95%	202	143
HMADZ55	939916	3071	blastx.2	(AK002022) unnamed protein product [Homo sapiens]	dbj BAA92041.1	98%	270	728
HMAFY42	778521	3078	HMMER 2.1.1	PFAM: WH1 domain	PF00568	90	46	303
HMAGK69	723186	3080	HMMER 1.8	PFAM: Signal C terminal domain	PF00512	40.87	31	405
HMAIC22	947905	3085	HMMER 2.1.1	PFAM: Peptidase family M3	PF01432	65.9	115	402
HMAKA11	966282	9569	blastx.14	CG Site No. 18031 [Escherichia coli]	gi 466635 gb AAB18474.1	84%	112	390
						100%	2	112
						55%	363	422
HMAKA11	966282	9569	blastx.14	MaoB [Escherichia coli]	gi 1480003 dbj BAA11058.1	99%	1516	803
						90%	1673	1545
HMALL66	956195	3091	HMMER 1.8	PFAM: Adenylate kinases	PF00406	50.17	1587	1474
HMCDN22	895981	3107	blastx.2	(AJ007798) stromal antigen 3, (STAG3) [Homo sapiens]	emb CAB59367.1	82%	85	456
						90%	445	573
HMCFB22	963794	3110	blastx.14	probable transposase - human transposon MER37	pir S72481 S72481	71%	10	168
						73%	183	320
						82%	119	187
HMCYG77	753133	3117	HMMER 2.1.1	PFAM: Kelch motif	PF01344	43%	313	423
						61%	5	58
HMMAB49	462502	3127	HMMER	PFAM: Zinc-binding	PF00099	63%	90	122
						51.9	7	132
						3.49	166	183

HMMAC19	953580	3129	1.8 blastx.14	metalloprotease domain (AF003535) ORF2-like protein [Homo sapiens]	gi 2197085 gb AAD0 4635.1	47% 47% 87%	26 282 187	145 344 210
HMMCH04	944069	3208	blastx.2	unknown [Homo sapiens]	gb AAC50940.1	58%	423	680
HMQBU96	765162	3247	HMMER 1.8	PFAM: Helix-loop-helix DNA-binding domain	PF00010	7.33	8	40
HMQDZ19	940694	3267	blastx.14	urokinase plasminogen activator receptor [Homo sapiens]	gi 433901 emb CAA5 2191.1	100% 91%	89 133	124 168
HMSBV28	970579	3303	blastx.14	YKL249 [Saccharomyces cerevisiae]	gi 871536 emb CAA4 9304.1	92% 51% 50%	260 141 323	108 1 282
HMSCD15	918133	3310	HMMER 1.8	PFAM: Src homology domain 3	PF00018	41.06	453	599
HMSFR69	738588	3373	blastx.2	(AK000975) unnamed protein product [Homo sapiens]	dbj BAA91451.1	98% 29% 28%	453 387 80	635 479 175
HMSGGL27	855759	9573	HMMER 1.8	PFAM: Core histones H2A, H2B, H3 and H4	PF00125	7.78	258	202
HMSGP73	925385	3401	HMMER 1.8	PFAM: Bacterial mutT protein	PF00293	5.56	276	202
HMSGX14	871492	3413	blastx.14	(AC004490) R29381_1 [Homo sapiens]	gi 2995577 gb AAC0 8316.1	94% 95%	141 901	908 972
HMSHO64	746582	3431	HMMER 1.8	PFAM: Ribosomal protein S12	PF00164	33.44	28	153
			blastx.2	PFAM: Src homology domain 3	PF00018	11.08	316	405
				(AF030131) Plenty of SH3s; POSH [Mus]	gb AAC40070.1	47%	1	411

HMSHZ56	733386	3447	HMMER 1.8	musculus] PFAM: Zinc finger, CCHC class	PF00098	4.89	208	228
HMSJT11	965007	3491	blastx.14	(AF148805) latent nuclear antigen [Kaposi sarcoma- associated herpesvirus]	gi 5669894 gb AAD4 6501.1 AF148805_6	20% 24% 21% 23% 16%	667 241 241 211 139	1137 465 465 453 465
HMSJW19	744990	3498	HMMER 2.1.1	PFAM: BAH domain	PF01426	48.7	2	163
HMSKI08	959413	3509	blastx.14	(AF094516) E1-like protein [Homo sapiens]	gi 3820614 gb AAC6 9630.1	97%	97	513
HMSOM08	958216	3538	blastx.14	(AF082556) TRF1 - interacting ankyrin-related ADP-ribose polymerase [Homo sapiens]	gi 3929219 gb AAC7 9841.1	76%	2	232
HMSOU92	948130	9578	blastx.2	(AF118082) PRO1902 [Homo sapiens]	gb AAF22026.1 AF1 18094_21	64% 63% 88%	302 462 532	463 527 558
HMSOX47	948202	3548	blastx.14	cDNA EST EMBL:M89462 comes from this gene; cDNA EST 1 1 yk349d7.5 comes from this gene; cDNA EST yk358b9.5 comes from this	gi 3879085 emb CAA 94301.1	48% 39% 36% 39% 26%	514 365 266 173 514	612 463 355 256 591
HMVDU16	904807	3589	HMMER 1.8	PFAM: Core histones H2A, H2B, H3 and H4	PF00125	13.38	1252	1329
HMWCQ09	924634	3606	blastx.14	Emf1 alpha [Ephydatia muelleri]	gi 9300 emb CAA494 72.1	50% 33% 66%	19 99 217	84 233 243

HMWDD54	932261	3610	blastx.14	(AF175223) SANT domain protein SMRTER [Drosophila melanogaster]	gi 5815245 gb AAD52614.1 AF175223_1	38%	292	345
HMWDF88	906769	3612	HMMER 1.8	PFAM: Low-density lipoprotein receptor domain class A	PF00057	41.61	171	245
			blastx.14	(AF110520) NG29 [Mus musculus]	gi 4050096 gb AAC97969.1	69% 48% 35% 50%	114 129 9 72	239 239 110 107
HMWGG55	920575	3642	blastx.14	DNA polymerase [Pyrococcus furiosus]	gi 216918 dbj BAA02362.1	94%	195	308
HMWGT07	953454	3645	blastx.14	(AL078579) putative protein [Arabidopsis thaliana]	gi 4972120 emb CAB43977.1	40% 40% 46%	218 395 113	322 475 157
HMWHN70	851334	3654	HMMER 1.8	PFAM: Zinc finger, C3HC4 type (RING finger)	PF00097	6.51	187	255
HNEBJ08	958742	3689	blastx.14	mucin 2 precursor, intestinal - human (fragments)	pir A49963 A43932	35% 83%	305 320	264 303
HNEDU01	909832	3748	blastx.14	(AC002398) F25965_3 [Homo sapiens]	gi 2477513 gb AAB81198.1	71% 57% 62% 43% 50%	207 80 1 323 337	323 205 87 412 384
HNFEF95	971171	3792	blastx.14	ORF_o493 [Escherichia coli]	gi 606260 gb AAA58123.1	98% 89% 81%	548 103 185	201 20 105
HNFFM25	705856	3818	HMMER	PFAM: Laminin B	PF00052	0.47	520	603

HNFFT62	574623	3828	1.8	(Domain IV) PFAM: C2 domain	PF00168	2.74	207	272
HNFGI01	921431	3851	blastx.14 1.8	(AF118890) s-tomosyn isoform [Rattus norvegicus]	gi 4689231 gb AAD2 7819.1 AF118890_1	86% 100% 40%	234 153 287	302 200 361
HNFGI49	909707	3852	blastx.14	(AF086624) serine threonine kinase [Rattus norvegicus]	gi 3800869 gb AAC6 8900.1	100% 100%	1 60	45 86
HNFGM76	908665	3862	HMMER 2.1.1 blastx.2	PFAM: Zinc finger, C2H2 type (AF132599) RANTES factor of late activated T lymphocytes-1 [Homo sapiens]	PF00096 gb AAD26864.1 AF1 32599_1	74.8 92%	232 1	306 417
HNFHA11	967520	3874	HMMER 2.1.1 blastx.14	PFAM: Phosphoenolpyruvate carboxykinase phosphoenolpyruvate carboxykinase [Escherichia coli]	PF01293 gi 606337 gb AAA58 200.1	118.1 99%	55 55	219 360
HNFBK77	576186	3890	HMMER 2.1.1 blastx.14	PFAM: Aldehyde dehydrogenase family serine/threonine kinase with SH3 domain, leucine 1	PF00171 gi 758593 emb CAA8 8531.1	30.2 28% 46% 46% 25% 41%	231 248 43 371 79 176	326 331 81 415 186 211
HNFBQ01	938114	3897						
HNFBW14	939763	3908	HMMER 2.1.1	PFAM: Latrophilin/CL-1- like GPS domain	PF01825	35.1	44	196

			blastx.2	(AF166382) serpentine receptor [Mus musculus]	gb AAF00617.1 AF1 66382.1	44%	38	283
HNF1G07	918389	3921	blastx.14	(AF128881) PI3 kinase regulatory subunit P101 [Homo sapiens]	gi 4928058 gb AAD3 3397.1 AF128881_1	80% 60%	2 448	445 477
HNF1P50	965283	3936	blastx.14	mutant sterol regulatory element binding protein-2 1	gi 841318 gb AAA85 718.1	65% 34% 85%	356 42 665	631 128 685
HNGAL92	953889	3976	blastx.14	phosphatidylserine decarboxylase [Escherichia coli]	gi 551827 gb AAA83 896.1	73%	212	18
HNGAS51	773208	3984	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF000099	2.57	144	182
HNGBF80	574475	4001	HMMER 1.8	PFAM: Zinc finger, C2H2 type	PF000096	4.98	88	111
HNGBH77	577361	4005	HMMER 1.8	PFAM: ATP synthase A chain	PF00119	9.81	130	189
HNGCE85	970738	4039	blastx.14	hypothetical protein Tigger 2 - human transposon MER37.1	pir S72489 S72489	72% 63%	284 212	210 180
HNGCX07	953900	4065	HMMER 1.8	PFAM: Src homology domain 3	PF00018	3.68	45	161
HNGEN37	663955	4160	HMMER 2.1.1	PFAM: Indole-3-glycerol phosphate synthases	PF00218	125.4	2	223
HNGEQ07	953647	4169	HMMER 1.8	PFAM: TPR Domain	PF00515	10.86	164	238
HNGER43	699391	4173	HMMER 1.8	PFAM: Bacterial mutT protein	PF00293	3.79	151	195
HNGER96	922996	4177	blastx.14	Bkm-like protein [Drosophila melanogaster]	gi 552132 gb AAA28 872.1	60% 64%	250 250	294 291

HNGEW76	572874	4198	HMMER 1.8	PFAM: Helicases conserved C-terminal domain	PF00271	64%	250	291
HNGEX35	959230	4200	blastx.14	adenine phosphoribosyltransferase [Escherichia coli]	gi 1773151 gb AAB4 0223.1	75%	215	250
HNGEX95	572897	4202	HMMER 1.8	PFAM: Zinc finger, C2H2 type	PF00096	80%	28	57
HNGFG22	573084	4224	HMMER 1.8	PFAM: Bacterial regulatory proteins, luxR family	PF00196	4.66	194	247
HNGFG69	926873	4227	blastx.14	collagen [Ascaris suum]	gi 159657 gb AAA29 371.1	98%	205	366
HNGFK28	544726	4234	HMMER 1.8	PFAM: ABC transporters	PF00005	5.32	196	219
HNGFK28	566798	9584	HMMER 1.8	MsbA protein. [Escherichia coli]	dbj BAA35658.1	9.2	166	240
HNGFK28	943114	9585	HMMER 1.8	MsbA protein. [Escherichia coli]	dbj BAA35658.1	44%	228	175
HNGFK28	943114	9585	HMMER 1.8	PFAM: ABC transporters	PF00005	40%	145	80
HNGFK28	943114	9585	HMMER 1.8	PFAM: ABC transporters	PF00005	40%	145	80
HNGFK28	943114	9585	HMMER 1.8	PFAM: ABC transporters	PF00005	40%	307	248
HNGFK28	943114	9585	HMMER 1.8	PFAM: ABC transporters	PF00005	50%	67	38
HNGFK28	943114	9585	HMMER 1.8	PFAM: ABC transporters	PF00005	86.07	445	654
HNGFK28	943114	9585	HMMER 1.8	PFAM: ABC transporters	PF00005	100%	1	651
HNGFK28	943114	9585	HMMER 1.8	PFAM: ABC transporters	PF00005	86%	654	989
HNGFK28	943114	9585	HMMER 1.8	PFAM: ABC transporters	PF00005	86.07	445	654
HNGFK28	943114	9585	HMMER 1.8	PFAM: ABC transporters	PF00005	100%	1	651
HNGFK28	943114	9585	HMMER 1.8	PFAM: ABC transporters	PF00005	100%	654	989
HNGFK28	943114	9585	HMMER 1.8	PFAM: ABC transporters	PF00005	117.67	342	1
HNGFK28	943114	9585	HMMER 1.8	PFAM: ABC transporters	PF00005	100%	165	503

				[Escherichia coli]			84%	25	162
HNGFK28	943115	9586	HMMER 2.1.1	PFAM: ABC transporter transmembrane region.	PF00664		91%	2	37
			blastx.2	MsbA protein. [Escherichia coli]					
HNGFO46	935135	4244	blastx.14	hypothetical protein T23G5.2 - Caenorhabditis elegans	pir S28303 S28303		44%	84	10
						60%	116	87	
HNGFO81	526792	4246	HMMER 2.1.1	PFAM: Integrase core domain	PF00665		40%	205	161
						36%	263	198	
HNGFU12	971170	4265	HMMER 1.8	PFAM: RNase H	PF00075		42.7	84	215
			blastx.14	reverse transcriptase (476 AA) [Woolly monkey sarcoma virus]	gi 930259 emb CAA3 3367.1	55.68	102	290	
HNGFW09	924693	4270	blastx.14	180 kDa bullous pemphigoid antigen 2/type XVII collagen [Homo sapiens]	gi 1877435 gb AAB5 1499.1		44%	96	422
						60%	1	75	
HNGFW09							50%	196	155
							53%	167	129
							66%	155	129
							36%	75	1
							75%	152	129
							60%	335	306
							85%	152	132
							85%	152	132
							60%	196	167
							54%	196	164
							50%	289	248
							26%	131	63
							62%	152	129
							75%	152	129

HNGGH78	924908	4306	blastx.14	type VII collagen [Cricetulus griseus]	gi 388625 gb AAA36 968.1	75% 66% 66% 60%	152 155 155 193	129 129 129 164
						50% 34% 42% 40% 50% 58% 38% 41% 50%	356 47 285 288 171 171 6 53 171	397 115 341 347 206 206 59 103 206
HNGGM10	964819	4317	HMMER 1.8	PFAM: Laminin B (Domain IV)	PF00052	0.51	424	441
HNGGR74	765698	4340	HMMER 1.8	PFAM: Zinc finger, C2H2 type	PF00096	6.36	14	58
HNGHT06	935706	4450	blastx.14	unknown protein [Homo sapiens]	gi 1196398 gb AAA8 8020.1	50%	254	177
HNGIJ01	916748	4483	blastx.14	ORF2 [Rattus norvegicus]	gi 56588 emb CAA37 645.1	50% 57% 57%	168 280 73	293 342 114
HNGKE07	952221	4630	blastx.14	collagen type VII [Homo sapiens]	gi 495866 gb AAA58 965.1	58% 55% 47% 64% 57% 32% 33% 62%	336 93 155 327 266 87 81 355	286 40 105 286 225 13 1 332
HNGLE52	835972	4662	HMMER	PFAM:	PF00049	6.75	286	318

HNGLG06	839088	4666	1.8	Insulin/IGF/Relaxin family	PF000005				
			HMMER 1.8	PFAM: ABC transporters		47.92	348	599	
			blastx.2	Hypothetical protein HI0658 [Escherichia coli]	dbj BAA35501.1	99%	270	665	
HNGLH82	954140	4668	blastx.14	diaminopimelate decarboxylase [Escherichia coli]	gi 455170 gb AAA83861.1	38%	288	569	
						98%	416	249	
						71%	193	47	
						63%	258	136	
HNGMM87	806036	4715	HMMER 1.8	PFAM: ATP synthase A chain	PF00119	8.41	237	362	
HNGOO22	953888	4762	blastx.14	(AE000449) putative xylanase [Escherichia coli]	gi 1790156 gb AAC76742.1	94%	104	3	
						91%	151	116	
HNHAI11	967668	4790	blastx.14	p15E carboxyterminal sequence [Kirsten murine sarcoma virus]	gi 4469304 emb CAA25493.1	38%	262	161	
						28%	406	323	
						53%	310	272	
HNHBE19	724404	4798	HMMER 1.8	PFAM: Helicases conserved C-terminal domain	PF00271	4.4	113	145	
HNHBY45	774280	4823	HMMER 1.8	PFAM: ATP synthase A chain	PF00119	8.4	228	347	
HNHDM74	506621	4878	HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding domain	PF00130	1.89	395	427	
HNHDY50	924211	4910	blastx.14	unknown protein [Homo sapiens]	gi 1196398 gb AAA88020.1	50%	33	170	
						44%	23	169	
						41%	6	164	
HNHEJ85	964882	4955	blastx.14	synexin - bovine (fragment)	pir A27695 A27695	54%	47	15	
						46%	91	53	

HNHET25	953410	5002	blastx.14	(AJ005562) SPR2D protein [Mus musculus]	gi 30933363 emb CAA06591.1	40% 38%	114 91	85 53
HNHFA11	967126	5030	blastx.14	(AF144054) apoptosis related protein APR-4 [Homo sapiens]	gi 4868437 gb AAD31316.1 AF144054_1	52% 35%	212 342	355 401
HNHGD07	953416	5121	blastx.14	(AF053091) eyelid [Drosophila melanogaster]	gi 2981221 gb AAC06254.1	46% 55% 33% 30% 50% 36% 26% 62% 42% 62% 83%	164 227 295 259 346 268 259 367 322 367 367	241 280 384 384 381 333 384 390 378 390 384
HNHGE09	939727	5127	blastx.2	IDN4-GGTR14 PROTEIN.	sp Q9Y6Y5 Q9Y6Y5	81%	2	112
HNHGH20	959499	5146	blastx.14	notch4 [Homo sapiens]	gi 1841543 gb AAC63097.1	43% 77% 33% 33% 62%	56 154 256 297 131	9 128 167 244 108
HNHGV22	674653	5189	HMMER 1.8	PFAM: Helicases conserved C-terminal domain	PF00271	4.66	94	138
HNHHI10	964659	5251	blastx.14	ORF1 [Rattus norvegicus]	gi 56587 emb CAA37644.1	56% 34%	75 157	28 71

HNHHL74	765598	5266	HMMER 1.8		PFAM: Bacterial mutT protein	PF00293		33%	220	158
HNHIA95	908419	5318	HMMER 2.1.1		PFAM: gag gene protein p24 (core nucleocapsid protein)	PF00607		63%	187	155
								3.57	83	148
HNHPH29	934456	5496	blastx.14		(AF118275) atrophin- related protein ARP [Homo sapiens]			67.6	49	300
HOIAE91	935322	5497	HMMER 1.8		PFAM: Phorbol esters / diacylglycerol binding domain	PF00130		60%	363	407
								45%	14	73
HSATQ28	866951	5512	HMMER 1.8		PFAM: Ubiquitin carboxyl-terminal hydrolases family 2	PF00442		70%	91	120
								50%	262	297
HSAYN79	471037	5646	HMMER 1.8		PFAM: RNA recognition motif. (aka RRM, RBD, or RNP domain)	PF00076		4.12	360	380
HSYBL15	660053	5682	HMMER 1.8		PFAM: Phorbol esters / diacylglycerol binding domain	PF00130		22.31	2	70
HSYDP04	970789	5686	blastx.14		(AF113615) FH1/FH2 domain-containing protein FHOS [Homo sapiens]	gi 5106956 gb AAD3 9906.1 AF113615_1		100%	77	394
								50%	408	467
								47%	393	443
HT3SA07	954360	5702	blastx.14		ORF2 contains a reverse transcriptase domain.; ORF2 [Homo sapiens]	gi 339771 gb AAA51 622.1		50%	83	178
								54%	47	79
HT4GJ85	909971	5714	HMMER		PFAM: PH (pleckstrin	PF00169		11.11	365	451

			1.8	homology) domain				
			blastx.14	(AF053974) SWAP-70 [Mus musculus]	gi 3290154 gb AAC4 0155.1	53%	251	448
HTSEA69	952359	5721	blastx.14	(AL032624) cDNA EST yk321h8.5 comes from this gene; 1 from this gene [Caenorhabditis elegans]	gi 3881086 emb CAA 21522.1	88% 33%	4 448	54 492
HTAAW46	719422	5735	HMMER 1.8	PFAM: HMG (high mobility group) box	PF00505	37% 30%	264 123	479 251
HTABG87	940153	5745	HMMER 1.8	PFAM: Eukaryotic protein kinase domain	PF00069	5.82	6	35
			blastx.14	(AF006064) protein kinase homolog [Fowlpox virus]	gi 2393890 gb AAC5 8236.1	13.81	240	335
HTACW17	961560	5760	blastx.14	(AC007660) unknown protein [Arabidopsis thaliana]	gi 4895220 gb AAD3 2806.1 AC007660_7	54% 33%	8 189	139 356
HTAFE69	944409	5797	blastx.2	(AK000496) unnamed protein product [Homo sapiens]	dbj BAA91205.1	37% 61%	54 212	221 265
HTAHL45	908949	5817	HMMER 2.1.1	PFAM: SCAN domain	PF02023	69%	432	704
			blastx.14	(AC004522) Zn-finger- like protein; similar to Z98745 (PID:g2924250) [Homo sapiens]	gi 3006231 gb AAC0 9486.1	228.7	268	555
HTAHV04	926747	5826	blastx.14	(AC005757) R32611_1 [Homo sapiens]	gi 3688089 gb AAC6 2258.1	65% 36%	220 529	534 642
HTAJN08	958057	5841	HMMER	PFAM: Helicases	PF00271	100%	3	446
						5.49	20	55

HTDAE43	971582	9597	1.8	conserved C-terminal domain	gi 4868437 gb AAD31316.1 AF144054_1	53%	526	296
HTGCH58	909849	5895	HMMER 2.1.1	PFAM: RhoGAP domain	PF00620	91.4	420	797
			blastx.14	carboxyl terminus of the predicted protein shows 1 comes from this gene; cDNA EST EMBL:D32994 comes from this gene	gi 3874826 emb CAA86318.1	37% 44% 61%	420 657 771	605 758 809
HTGDM65	967158	5918	blastx.14	SH3 domain binding protein [Rattus norvegicus]	gi 1185397 gb AAA87791.1	39% 50% 39% 47% 39% 28% 40%	127 186 278 186 278 337 260	59 139 210 136 210 263 195
HTGDT91	974962	5921	HMMER 2.1.1	PFAM: SpoU rRNA Methylase family	PF00588	107.6	315	638
			blastx.14	alternate gene name yibK [Escherichia coli]	gi 466744 gb AAB18583.1	100% 100% 76% 81%	315 531 457 497	467 638 495 529
HTGDW96	967030	5926	HMMER 2.1.1	PFAM: Domain of unknown function	PF01784	130.2	334	711
			blastx.14	(AL034490) similar to yeast ngg1-interacting factor 3	gi 4008560 emb CAA22481.1	60% 43% 37%	1087 460 385	1275 660 513

HTGEL46	685425	5936	HMMER 1.8	[Schizosaccharomyces pombe]	PF00130	61%	361	414
				PFAM: Phorbol esters / diacylglycerol binding domain		28%	970	1065
						58%	1312	1347
HTGEQ11	967047	5944	HMMER 2.1.1 blastx.14	PFAM: Cytosol aminopeptidase family	PF00883	7.26	398	433
				aminopeptidase A [Escherichia coli]	gi 1054725 emb CAA 60164.1	95%	27	305
						83%	320	391
						88%	1	27
HTGER72	683469	5949	HMMER 1.8	PFAM: Src homology domain 3	PF00018	2.4	174	203
HTGFZ03	923443	5968	HMMER 2.1.1 blastx.14	PFAM: RNA polymerase beta subunit (AF025424) RNA polymerase I 127 kDa subunit [Rattus norvegicus]	PF00562	30.7	21	110
					gi 2739048 gb AAB9 4600.1	76%	3	275
HTGGL23	974590	5973	blastx.14	(AE000218) putative adhesion and penetration protein [Escherichia coli]	gi 1787452 gb AAC7 4286.1	87%	3	443
HTHCB68	660309	5996	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	3	162	209
HTJAB35	880424	9601	HMMER 1.8	PFAM: Ank repeat	PF00023	35.64	242	325
HTJMT23	948518	6056	blastx.14	(AF182426) arylacetamide deacetylase [Rattus norvegicus]	gi 5923874 gb AAD5 6394.1 AF182426_1	58%	2	160
HTOAK34	966800	6081	HMMER	PFAM: Eukaryotic protein	PF00069	32.41	1020	1190

			1.8 blastx.14	kinase domain (AF084205) serine/threonine protein kinase TAO1 [Rattus norvegicus]	gi 3452473 gb AAC7 1014.1	75%	954	1190
HTODG16	909952	6108	HMMER 2.1.1 blastx.14	PFAM: RasGEF domain	PF00617	148.5	4	402
				CDC25 [Saccharomyces kluuyveri]	gi 171187 gb AAA34 479.1	34%	13	399
HTOFT34	527144	6146	HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding domain	PF00130	4.53	235	264
HTOHL35	537364	6173	HMMER 1.8	PFAM: Zinc finger, C2H2 type	PF00096	6.52	4	33
HTOIY09	836003	6201	HMMER 1.8	PFAM: Insulin/IGF/Relaxin family	PF00049	7.08	61	123
HTSHF47	720403	6229	HMMER 1.8	PFAM: Helix-loop-helix DNA-binding domain	PF00010	7.82	105	140
HTSHM38	972248	6230	HMMER 2.1.1 blastx.14	PFAM: EGF-like domain (AB011532) MEGF6 [Rattus norvegicus]	PF00008 gi 3449294 dbj BAA3 2462.1	72 88% 50% 53% 42% 42% 43% 40% 46% 70% 66%	299 287 278 320 299 287 290 341 287 114 413	406 538 460 466 460 442 427 481 415 173 457

50%	467	532
61%	245	283
35%	188	280
47%	482	538
52%	245	295
39%	476	544
61%	245	283
31%	188	283
50%	245	286
29%	170	280
55%	230	283
69%	245	283
53%	245	283
50%	485	532
35%	452	535
47%	482	532
47%	482	532
50%	245	304
31%	299	412
70%	251	280
58%	251	286
30%	434	532
58%	245	280
53%	245	283
37%	245	316
63%	317	349
75%	245	268
47%	245	295
37%	251	322
54%	251	283
31%	320	406

36%	230	286
40%	401	460
60%	203	232
54%	473	505
34%	308	376
50%	245	280
25%	329	445
62%	245	268
37%	485	532
29%	251	343
50%	227	262
45%	251	283
24%	296	406
71%	485	505
40%	473	532
33%	344	406
71%	359	379
50%	245	280
60%	454	483
62%	245	268
33%	491	544
33%	320	382
63%	344	376
62%	359	382
71%	203	223
45%	203	235
37%	215	262
37%	359	406
38%	356	409
36%	320	376
40%	320	379

HTWCG65	869547	6260	HMMER 1.8	PFAM: Core histones H2A, H2B, H3 and H4	PF00125	60%	251	280
HTWEY30	918641	6299	blastx.14	(AF036548) RGC-32 [Rattus norvegicus]	gi 3800742 gb AAC6 8839.1	15.45	220	306
HTWJA59	812705	6314	HMMER 1.8	PFAM: Helicases conserved C-terminal domain	PF00271	88%	613	434
HTXCY84	924996	6359	HMMER 2.1.1	PFAM: Aldehyde dehydrogenase family	PF00171	4.95	172	219
HTXDW14	966588	6366	blastx.14	(AF038838) proline dehydrogenase [Klebsiella aerogenes]	gi 2766693 gb AAB9 5478.1	23.9	104	217
HTXDX61	784768	6367	HMMER 2.1.1	(AB029335) HrPET-3 [Halocynthia roretzi]	gi 5360271 dbj BAA8 1908.1	78%	47	241
HTXFN69	869397	6394	HMMER 1.8	PFAM: Amidase	PF01425	45%	16	48
HTXGL73	529745	6403	HMMER 1.8	PFAM: HMG (high mobility group) box	PF00505	41%	20	70
HTXJL68	912611	6420	blastx.14	PFAM: Phorbol esters / diacylglycerol binding domain	PF00130	54%	869	777
HTXJM73	783572	6425	HMMER 1.8	RAB14 [Rattus norvegicus]	gi 206535 gb AAA41 994.1	45%	773	663
HTXKQ55	947789	6453	HMMER 2.1.1	PFAM: Bacterial mutT protein	PF00293	123.2	61	330
				PFAM: Peptidase family M3	PF01432	6.76	72	137
						2.21	144	176
						97%	230	370
						60%	367	450
						59%	482	547
						52%	373	429
						2.87	97	123
						50.1	3	299

			blastx.14	mitochondrial intermediate peptidase precursor [Homo sapiens]	gi 1763642 gb AAC51231.1	96% 100%	3 335	302 367
HTXNY74	918076	6525	blastx.14	(AF078856) p47 [Homo sapiens]	gi 5531827 gb AAD44488.1	89% 96%	93 2	530 94
HTXPT68	870074	6555	HMMER 2.1.1	PFAM: NOL1/NOP2/sun family	PF01189	43.1	29	196
HTXQC36	961161	6560	blastx.14	(AB012223) ORF2 [Canis familiaris]	gi 2981631 dbj BAA25253.1	51% 57% 60% 42%	9 326 145 170	143 382 174 247
HTXRM86	975072	6575	HMMER 2.1.1	PFAM: Prokaryotic DNA topoisomerase	PF01131	99	243	446
HTXSB88	914627	6577	blastx.14	DNA topoisomerase III (EC 5.99.1.-) [Escherichia coli]	gi 1742870 dbj BAA15551.1	51% 40%	177 3	440 158
HTXSR92	973095	6579	blastx.2	(AF077042) 30S ribosomal protein S7 homolog [Homo sapiens]	gi 4689132 gb AAD27775.1 AF077042_1	84%	559	771
HUJAM39	911399	6586	blastx.14	(AB016962) synGAP-b1 [Rattus norvegicus]	dbj BAA74972.1	60% 55%	302 1	421 60
HUJCM08	957784	6589	blastx.14	(AF051325) SH3 domain containing adaptor protein [Homo sapiens]	gi 4091782 gb AAC99298.1	46% 32%	170 709	310 885
HUJAV06	966816	6597	blastx.14	(AF015950) telomerase reverse transcriptase [Homo sapiens]	gi 2330017 gb AAC51672.1	100%	2	244
			blastx.14	(AF151854) CGI-96 protein [Homo sapiens]	gi 4929661 gb AAD34091.1 AF151854_1	88% 100% 68% 36%	595 464 537 561	521 396 481 487

HWAAF66	908541	6612	HMMER 2.1.1 blastx.14	PFAM: KRAB box repressor protein [Homo sapiens]	PF01352 gi 2789430 dbj BAA24380.1	65.3	90	278
HWAAAY03	923734	6619	HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding domain	PF00130	2.21	332	373
HWACA38	943074	6637	HMMER 1.8 blastx.14	PFAM: Bacterial mutT protein (AL033536) predicted using Genefinder; similar to 1 1 1 elegans]	PF00293 gi 3947651 emb CAA22138.1	3.68 39% 52%	344	376 433 834
HWADF26	957347	6656	HMMER 1.8 blastx.2	PFAM: Lectin C-type domain short and long forms (AF175206) lectin-like receptor F1 [Homo sapiens]	PF00059 gb AAAF37804.1 AF175206_1	104.26 100%	859 3	509 596
HWAEN20	868490	6691	HMMER 1.8	PFAM: Zinc finger, C2H2 type	PF00096	6.01	251	313
HWAFW39	947915	6697	HMMER 2.1.1 blastx.2	PFAM: Peptidase family M1 (AF106037) adipocyte-derived leucine aminopeptidase [Homo sapiens]	PF01433 gb AAAF07395.1 AF106037_1	79.5 96%	200 200	367 367
HWAFX39	907631	6698	blastx.14	Zn-binding protein [Pleurodeles waltl]	gi 213868 gb AAA49614.1	46% 50%	118 19	354 120
HWAGM33	888685	6710	HMMER 2.1.1	PFAM: Plexin repeat	PF01437	25.8	898	1035

HWAGX37	959586	6711	blastx.14	unknown protein [Homo sapiens]	gi 1196433 gb AAA88038.1	47%	215	283
						34%	535	639
						42%	409	471
						29%	295	396
HWAHI10	960646	6714	blastx.14	retinoid X receptor interacting protein [Mus musculus]	gi 709961 gb AAC52167.1	62%	1215	583
						66%	513	343
						45%	642	412
						44%	1272	1198
						66%	1824	1798
HWAHS94	909667	6715	blastx.14	(AF151363) Cdc42 GTPase-activating protein [Mus musculus]	gi 5020264 gb AAD38043.1 AF151363_1	63%	278	484
						75%	487	510
HWBAL44	959449	6720	blastx.14	(AF151877) CGI-119 protein [Homo sapiens]	gi 4929707 gb AAD34114.1 AF151877_1	100%	531	424
HWBAQ16	868363	6722	HMMER 1.8	PFAM: RNA recognition motif. (aka RRM, RBD, or RNP domain)	PF000076	4.8	857	898
HWBBR65	747723	6741	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF000099	4.15	185	205
HWBDM24	963498	6771	blastx.14	(AJ388555) hypothetical protein [Canis familiaris]	gi 5441611 emb CAB46854.1	83%	908	997
						100%	990	1040
						88%	837	863
HWBEX27	682583	6785	HMMER 1.8	PFAM: Helix-loop-helix DNA-binding domain	PF00010	38.64	184	336
HYAAF33	915050	6820	blastx.14	(AF121858) sorting nexin 8 [Homo sapiens]	gi 4689256 gb AAD27831.1 AF121858_1	81%	273	434
						96%	217	306
						36%	172	270
HYAAS08	926017	6831	blastx.14	ORF-3 protein [Pseudorabies virus]	gi 334072 gb AAA47471.1	62%	203	156
						34%	84	7
						36%	125	69
						63%	150	118

HYABP53	971448	6848	HMMER 2.1.1	PFAM: Immunoglobulin domain	PF00047	37%	282	211
HYABB43	800006	6860	HMMER 2.1.1	PFAM: Alpha-2- macroglobulin family	PF00207	90.9	206	27
			blastx.2	alpha-2-macroglobulin [Mus musculus]	gb AAA39508.1	67%	263	36
HYAAU65	909956	6863	HMMER 2.1.1	PFAM: RasGEF domain	PF00617	47	2	112
HWBEG18	909798	6883	HMMER 2.1.1	PFAM: EF hand	PF00036	33.3	505	591
			blastx.14	(AF106071) ras activator RasGRP [Homo sapiens]	gi 4038292 gb AAC9 7349.1	71% 59% 46% 70% 48% 66%	698 382 103 604 2 619	889 597 420 684 142 654
			HMMER 2.1.1	PFAM: B-box zinc finger.	PF00643	32.5	263	388
			blastx.14	(AF119043) transcriptional intermediary factor 1 gamma; TIF1 gamma [Homo sapiens]	gi 4325109 gb AAD1 7259.1	92%	2	562
HWBAQ71	944080	6918	blastx.2	predicted using GeneFinder [Caenorhabditis elegans]	emb CAA97423.1	34%	141	464
HWAFG12	969605	6934	blastx.14	(AF071081) proline-rich mucin homolog [Mycobacterium tuberculosis]	gi 5305335 gb AAD4 1594.1 AF071081_1	34% 50% 28% 40%	112 195 398 365	17 142 264 300

HWAFA47	948858	6938	blastx.2	(AF010144) neuronal thread protein AD7c-NTP [Homo sapiens]	gb AAC08737.1	34%	219	142
						44%	154	101
						32%	374	300
						34%	365	297
						34%	332	264
						63%	338	306
						29%	365	294
						38%	314	261
						59%	208	14
						50%	178	14
HWAUE35	887166	6942	HMMER 2.1.1 blastx	PFAM: Immunoglobulin domain CMRF-35 antigen [Homo sapiens]	PF00047 emb CAA46948.1	40%	253	80
						77%	78	13
						52%	93	25
						76%	249	211
						42%	221	165
						75%	240	205
						42%	237	160
						90%	357	328
						25%	248	168
						23.2	40	273
HWAEG71	931547	6946	HMMER 1.8 blastx.2	PFAM: Ras family (contains ATP/GTP binding P-loop) rab-related GTP-binding protein [Rattus	PF00071 gb AAA42000.1	55%	7	162
						59%	169	279
						60%	400	474
						38%	346	399
						42%	316	372
						147.95	116	475
						98%	86	493
						80%	477	569

HWAEC08	958115	6947	HMMER 2.1.1	norvegicus] PFAM: Spectrin repeat	PF00435	29.5	3	215
HWACY70	756888	6956	HMMER 2.1.1	(AL080133) hypothetical protein [Homo sapiens]	gi 5262574 emb CAB 45729.1	69%	12	209
						70%	381	452
						31%	18	209
						29%	228	308
HWABG11	949088	6971	HMMER 2.1.1	PFAM: RIO1/ZK632.3/MJ0444 family	PF01163	96	280	552
HUUDR34	944903	6984	HMMER 2.1.1	PFAM: Glucosamine-6- phosphate isomerase	PF01182	225.7	67	381
HUUCJ02	940813	6986	blastx.14	unnamed protein product [unidentified]	emb CAA03416.1	91%	67	480
HUUCJ02	940813	6986	blastx.14	(AF132984) nuclear pore complex interacting protein NP1P [Homo sapiens]	gi 4826478 emb CAB 42896.1	82%	2	550
						100%	571	594
						77%	552	578
						100%	596	616
						99%	770	417
						89%	417	250
						71%	300	187
						58%	226	119
						87%	278	231
						100%	261	226
HUUCJ02	940813	6986	blastx.14	(AF132984) nuclear pore complex interacting protein NP1P [Homo sapiens]	gi 4959568 gb AAD3 4394.1 AF132984_1	54%	261	196
						60%	258	199
						81%	181	149
						83%	152	117
						40%	229	149
						100%	152	126
						90%	192	163

HTXOO15	869261	7011	HMMER 2.1.1	PFAM: Ubiquitin family	PF00240	66%	300	274
HTXLS08	958357	7023	blastx.14	(AF090989) high-risk human papilloma viruses E6 1 alpha [Homo sapiens]	gi 4151328 gb AAD1 2543.1	48% 68% 41% 57% 70% 27%	745 1006 1 511 427 580	987 1146 237 645 477 645
HTWKB07	952841	7085	blastx.14	(AF003535) ORF2-like protein [Homo sapiens]	gi 2197085 gb AAD0 4635.1	60% 75% 50% 33% 70%	25 259 205 36 167	84 294 258 116 196
HTWJH08	790185	7087	blastx.2	(AK000385) unnamed protein product [Homo sapiens]	dbj BAA91131.1	61%	197	51
HTWJH08	846554	9615	blastx.2	(AK000385) unnamed protein product [Homo sapiens]	dbj BAA91131.1	61%	197	51
HTWJF50	911448	7089	blastx.14	myosin I [Rattus norvegicus]	gi 3724141 emb CAA 50871.1	48% 53% 55% 46% 39% 50%	1009 334 732 863 40 686	1428 681 851 1012 108 715
HTWFQ19	586124	7091	HMMER 2.1.1	PFAM: Sema domain	PF01403	62.9	14	184
HTOIA82	844319	7198	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	4.25	50	82
HTOHI14	659280	7204	HMMER	PFAM: Asparaginase	PF01112	20.7	140	217

HTODM08	960113	7222	2.1.1 blastx.14	(AF106069) deubiquitinating enzyme [Homo sapiens]	gi 5814097 gb AAD5 2099.1 AF106069_1	33%	5	367
HTHBY73	946168	7282	blastx.2	(AK001868) unnamed protein product [Homo sapiens]	dbj BAA91951.1	52% 45%	4 162	183 332
HTGEX10	963862	7305	HMMER 2.1.1	PFAM: SET domain	PF00856	105.2	580	960
HTGEA37	908606	7311	blastx.14	(AC005065) determined by GENSCAN prediction and 1	gi 4153862 gb AAD0 4721.1	65% 40%	601 337	1017 477
HTAIF22	910040	7364	HMMER 2.1.1	(AF001293) aiolos [Mus musculus]	gi 2150044 gb AAB5 8795.1	80%	1	216
			blastx.14	PFAM: RhoGEF domain	PF00621	29.5	320	394
			blastx.14	(AL022271) similar to Guanine nucleotide exchange 1 1 1 this g	gi 3876654 emb CAA 18349.1	64%	281	397
HTAIF11	965738	7365	blastx.14	(AF061555) ubiquitin- protein ligase E3-alpha [Mus musculus]	gi 3170887 gb AAC4 0165.1	48% 50%	6 297	293 392
HTAEV23	959129	7369	HMMER 2.1.1	PFAM: WW domain	PF00397	25.9	478	386
			blastx.14	This gene is novel. [Homo sapiens]	gi 603953 dbj BAA07 893.1	89%	823	359
HTAEP05	932459	7370	blastx.14	Pro-Pol-dUTPase polyprotein [Mus musculus]	gi 2065210 emb CAA 73251.1	76% 48% 47% 44%	225 406 3 500	275 510 59 553

HTABK47	720684	7379	HMMER 2.1.1	PFAM: Monooxygenase	PF01360	77%	386	412
HSYCV01	940661	7408	HMMER 1.8	PFAM: Hydroxymethylglutaryl- coenzyme A reductase	PF00369	7.29	448	492
HSAWR08	959943	7458	blastx.14	(AL110271) hypothetical protein [Homo sapiens]	gi 5817084 emb CAB 53709.1	98%	123	287
HSAUL84	908440	7504	HMMER 2.1.1	PFAM: gag gene protein p24 (core nucleocapsid protein)	PF00607	43.3	105	302
HNHOF94	948720	7551	blastx.14	gag protein [Human endogenous retrovirus K.]	gi 1780975 emb CAA 71418.1	83%	135	299
			blastx.2	(AK000496) unnamed protein product [Homo sapiens]	dbj BAA91205.1	60%	24	152
HNHNP81	928378	7554	HMMER 1.8	PFAM: 7 transmembrane receptor (rhodopsin family)	PF00001	58.09	233	511
			blastx.2	(AF091575) olfactory receptor [Rattus norvegicus]	gb AAC64595.1	61%	236	505
HNHLC01	915363	7581	blastx.14	unknown protein [Homo sapiens]	gi 1196431 gb AAA8 8036.1	52%	502	618
			blastx.2	(AK000385) unnamed protein product [Homo sapiens]	dbj BAA91131.1	46%	5	82
HNHGV62	743400	7603	blastx.2			40%	57	131
						36%	133	207
						61%	219	257
						46%	260	304
						62%	52	285
						76%	287	349

HNHGE31	698046	7624	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	3.3	83	109
HNHFV49	975415	7644	blastx.2	hypothetical protein (L1H 3' region) - human	pir B34087 B34087	81% 71% 90%	483 227 217	190 6 188
HNHFH24	903741	7657	HMMER 2.1.1	PFAM: Sodium:neurotransmitter symporter family	PF00209	37.2	208	306
			blastx.14	(AF075266) orphan transporter isoform B9 [Mus musculus]	gi 3347930 gb AAC2 7761.1	76% 27%	187 414	327 467
HNHDF07	953883	7702	HMMER 1.8	PFAM: Fibronectin type III domain	PF00041	7.48	242	319
HNHDC29	904546	7704	blastx.14	contactin associated protein [Homo sapiens]	gi 1857708 gb AAB4 8481.1	98%	219	7
HNHCI32	861673	7716	HMMER 1.8	PFAM: 7 transmembrane receptor (rhodopsin family)	PF00001	133.17	195	545
			blastx.2	(AF112461) G protein- coupled receptor 57 [Homo sapiens]	gb AAF27279.1 AF1 12461_1	100% 100% 100%	189 112 56	551 186 112
HNHCI32	956105	9645	HMMER 1.8	PFAM: 7 transmembrane receptor (rhodopsin family)	PF00001	133.17	951	601
			blastx.2	(AF112461) G protein- coupled receptor 57 [Homo sapiens]	gb AAF27279.1 AF1 12461_1	100% 100% 100%	555 478 422	917 552 478
HNHBF47	949027	7731	HMMER 1.8	PFAM: Cadherin	PF00028	44.76	668	522
			blastx.2	(AB028499) Flamingo 1	dbj BAA84070.1	96%	409	666

[illegible]

HNHAF61	742116	7745	HMMER 1.8	PFAM: Cadherin	PF00028		39%	412	480
			blastx.2	(AF152473) protocadherin alpha C1 short form protein [Homo sapiens]	gb AAD43734.1 AF1 52473_1		46.67	330	461
HNHAF61	955094	9649	blastx.14	(AF152303) protocadherin alpha C1 [Homo sapiens]	gi 5456892 gb AAD4 3697.1		75%	81	677
							84%	173	364
HNGOZ40	969158	7757	blastx.14	(AF155098) NY-REN-8 antigen [Homo sapiens]	gi 5360091 gb AAD4 2864.1 AF155098_1		33%	87	686
							93%	1	84
HNGNY02	918626	7769	HMMER 1.8	PFAM: FAD/NAD- binding domain in oxidoreductases	PF00175		40%	10	75
							98%	325	1071
HNGND01	915294	7778	HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding domain	PF00130		40%	715	987
							42%	499	660
HNGMW65	950173	7781	blastx.2	(AF010144) neuronal thread protein AD7c-NTP	gb AAC08737.1		32%	778	1023
							37%	724	867
							100%	225	275
							77%	176	229
							30%	496	684
							89%	269	325
							35%	895	1011
							40%	568	663
							36%	717	791
							50%	499	540
							78%	599	477
							4.43	366	440
							2.07	464	490
							62%	340	143
							67%	340	248

HNGMD48	974358	7788	HMMER 1.8	PFAM: Cystatin domain	PF00031	45% 60% 55% 68% 43% 43% 55% 64% 57% 47%	417 345 80 81 200 414 205 392 202 86	247 247 3 25 111 346 152 351 125 18
HNGLY08	948825	7791	blastx.14	(AJ010949) calcium channel alpha-2-delta-C subunit [Mus musculus]	gi 4186073 emb CAA 09423.1	79%	219	392
HNGLL07	952236	7795	blastx.14	KERATIN TYPE II CYTOSKELETAL 8 (FRAGMENT).	sp Q29386 Q29386	41% 71% 83% 72%	199 43 77 242	77 2 42 210
HNGKM74	942758	7801	HMMER 1.8 blastx.2	PFAM: HMG (high mobility group) box (AL117470) hypothetical protein [Homo sapiens]	PF00505 emb CAB55945.1	5.95 40%	437 2	526 817
HNGIR10	964715	7837	blastx.14	NK10 [Mus musculus]	gi 506502 emb CAA5 6225.1	61% 62% 54% 52% 54% 53% 50% 44%	196 193 199 196 193 199 193 196	2 2 2 2 2 2 2 8

HNGFF50	941480	7879	blastx.14	(AJ010949) calcium channel alpha-2-delta-C subunit [Mus musculus]	gi 4186073 emb CAA.09423.1	45%	193	2
						61%	199	92
						57%	196	83
						37%	178	11
						26%	217	2
						39%	115	2
						46%	181	104
						50%	232	197
						33%	309	256
						30%	306	238
						78%	285	130
						86%	986	921
HNGEO79	951489	7897	HMMER 1.8	PFAM: IG (immunoglobulin) superfamily	PF00047	33.71	290	466
			blastx	(AF143185) high affinity immunoglobulin gamma Fc 1	gb AAD34946.1 AF143185_1	54%	287	385
						41%	404	520
						77%	230	283
						36%	140	214
HNGEI11	967314	7902	blastx.14	pol polyprotein [Baboon endogenous virus]	gi 509838 gb AAA87332.1	70%	258	317
						42%	39	152
						53%	324	368
HNGDM11	967512	7933	blastx.14	reverse transcriptase [Homo sapiens]	gi 439877 gb AAB02291.1	36%	381	292
						50%	276	205
						47%	154	104
						20%	210	82
HNGDA08	959964	7952	HMMER 1.8	PFAM: Zinc finger, CCHC class	PF00098	5.01	261	284
HNGAZ08	959977	7973	blastx.14	p40 [Homo sapiens]	gi 2072966 gb AAC51272.1	45%	391	320
						40%	93	19

HNFID11	966347	7997	blastx.14	(AF132948) CGI-14 protein [Homo sapiens]		gi 4680667 gb AAD27723.1 AF132948_1	40%	144	100
HNFHR56	733297	8003	HMMER 1.8	PFAM: IG (immunoglobulin) superfamily		PF00047	100%	14	115
HNEDO77	955894	8051	blastx.14	(AB020063) Keap1 [Mus musculus]		gi 3894323 dbj BAA34639.1	90% 44% 42% 38% 44% 100% 27% 85%	384 387 420 339 387 79 402 360	64 91 91 91 232 44 316 346
HNEBJ81	529571	8067	HMMER 2.1.1	PFAM: N-acetyltransferase		PF00797	40.5	18	125
HMWEN61	909931	8125	blastx.14	(AF020313) proline-rich protein 48 [Mus musculus]		gi 2624972 gb AAB94880.1	84% 100%	89 89	307 9
HMWBT59	893995	8141	HMMER 1.8	PFAM: 4 transmembrane segments integral membrane proteins		PF00335	27.49	51	113
HMSMN71	927097	8184	HMMER 1.8	PFAM: Ubiquitin family		PF00240	32.11	24	200
			blastx.14	(AF176069) ubiquitin [Homo sapiens]		gi 5733824 gb AAD49751.1 AF176069_1	78% 63% 53%	3 550 550	518 606 594
HMSJL53	921263	8196	blastx.14	decorin (PGII) [Mus musculus]		gi 53669 emb CAA37876.1	36% 46% 35%	281 48 134	403 131 244